SEQUENCE LISTING

<110> Falco, Carl
Famodu, Layo O.
Orozco, Buddy
Rafalski, Antoni
Thorpe, Cathy

<120> Tetrahydrofolate Metabolism Enzymes

<130> BB1179 USDIV1

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<150> US 60/092,869
<151> 1998-07-15

<150> US 09/351,703
<151> 1999-07-12

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cgcccgctcc tcgtcgggga tntccaattc ggctgctaca atccttcggc gccaagctgt 480
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<210> 2
<211> 375
<212> PRT
<213> Zea mays

<400> 2

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Val Arg Ala Thr Arg Asp Thr Met Arg Arg Ser Leu Pro Leu Leu Leu
             20                  25                  30

Ala Arg Gln Val Ala Arg Gln Arg Arg Leu Ser Asn Val Pro Glu Ser
         35                  40                  45

Thr Val Tyr Gly Gly Pro Arg Pro Gln Glu Ser Ser Ala Ala Arg Arg
     50                  55                  60

Val Thr Val Thr Thr Leu Arg Gly Lys His Arg Arg Gly Glu Pro Ile
 65                  70                  75                  80

Thr Val Val Thr Ala Tyr Asp Tyr Pro Ser Ala Val His Val Asp Ser
                 85                  90                  95

Ala Gly Ile Asp Val Cys Leu Val Gly Asp Ser Ala Ala Met Val Val
            100                 105                 110

His Gly His Asp Thr Thr Leu Pro Ile Thr Leu Asp Ile Met Leu Glu
        115                 120                 125

His Cys Arg Ala Val Ala Arg Gly Ala Pro Arg Pro Leu Leu Val Gly
    130                 135                 140

Asp Leu Pro Phe Gly Cys Tyr Glu Ser Ser Ala Ala Gln Ala Val Asp
145                 150                 155                 160

Ser Ala Val Arg Val Leu Lys Glu Gly Gly Met Asp Ala Ile Lys Leu
                165                 170                 175

Glu Gly Gly Ala Pro Ser Arg Ile Thr Ala Ala Lys Ala Ile Val Glu
            180                 185                 190

Ala Gly Ile Ala Val Met Gly His Val Gly Leu Thr Pro Gln Ala Ile
        195                 200                 205

Ser Val Leu Gly Gly Phe Arg Pro Gln Gly Lys Thr Val Asp Ser Ala
    210                 215                 220

Ile Lys Val Val Glu Thr Ala Leu Ala Leu Gln Glu Ala Gly Cys Phe
225                 230                 235                 240

Ser Val Val Leu Glu Cys Val Pro Ala Pro Val Ala Ala Ala Ala Thr
                245                 250                 255

Ser Ala Leu Lys Ile Pro Thr Ile Gly Ile Gly Ala Gly Pro Phe Cys
            260                 265                 270

Ser Gly Gln Val Leu Val Tyr His Asp Leu Leu Gly Met Leu Gln His
        275                 280                 285

Pro His His Ala Lys Val Thr Pro Lys Phe Cys Lys Gln Phe Gly Asn
    290                 295                 300

Val Gly Asp Val Ile Asn Lys Ala Leu Ser Glu Tyr Lys Gln Glu Val
305                 310                 315                 320
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```
Glu Ala Gln Ala Phe Pro Gly Pro Ser His Thr Pro Tyr Lys Ile Thr
                325                 330                 335

Pro Thr Asp Val Asp Gly Phe Ala Asp Ala Leu Gln Lys Met Gly Leu
            340                 345                 350

Ser Asp Ala Ala Asp Ala Ala Ala Ala Ala Ala Glu Asn Arg Glu Lys
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Gly Gly Glu Pro Asn Gly Glu
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<210> 3
<211> 652
<212> DNA
<213> Zea mays

<220>
<221> unsure
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<223> n is a, c, g or t

<400> 3

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tacttaccca ccgcacctgc caacaaaaga gagaaagaga tcttggaatt gatccagggt 180
acagattttg ttgtgctggc aagatacatg cagatactct cagaaaacct gttaaaagca 240
tatggtaaag acattatcaa tattcatcat ggccttcttc cctcatttaa gggagggaat 300
ccttcaagac aggccttcag tgctggggtg aagttaatcg gggcaactag ccatttcgtt 360
actccagaac ttgatgctgg gccaatcatt gaacagatgg ttgaacgagt ctctcaccga 420
gacacgttac agagttttgt tgtcaagtct gagaaccttg agaagcagtg cttaacagaa 480
gctatcaagt catattgcga gcttcgtgtc taccatatga actcaggaag actgtcgtgg 540
tctgatctga gcttccttta ttttctggct taattggact tttatatggg attgntaaaa 600
tgaaattttt aactttaaat atattcattc ccctcgacaa ttattttaag gg         652
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<210> 4
<211> 169
<212> PRT
<213> Zea mays

<400> 4

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Leu Tyr Arg Trp Gln Glu Gly Arg Leu Pro Val His Ile Asn Cys Val
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Ile Ser Asn His Asp Arg Val Arg Arg Phe Leu Gln Arg His Gly Ile
             20                  25                  30

Pro Tyr His Tyr Leu Pro Thr Ala Pro Ala Asn Lys Arg Glu Lys Glu
         35                  40                  45

Ile Leu Glu Leu Ile Gln Gly Thr Asp Phe Val Val Leu Ala Arg Tyr
     50                  55                  60

Met Gln Ile Leu Ser Glu Asn Leu Leu Lys Ala Tyr Gly Lys Asp Ile
 65                  70                  75                  80

Ile Asn Ile His His Gly Leu Leu Pro Ser Phe Lys Gly Gly Asn Pro
                 85                  90                  95
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```
Ser Arg Gln Ala Phe Ser Ala Gly Val Lys Leu Ile Gly Ala Thr Ser
            100                 105                 110

His Phe Val Thr Pro Glu Leu Asp Ala Gly Pro Ile Ile Glu Gln Met
        115                 120                 125

Val Glu Arg Val Ser His Arg Asp Thr Leu Gln Ser Phe Val Val Lys
    130                 135                 140

Ser Glu Asn Leu Glu Lys Gln Cys Leu Thr Glu Ala Ile Lys Ser Tyr
145                 150                 155                 160

Cys Glu Leu Arg Val Tyr His Met Asn
                165
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<210> 5
<211> 563
<212> DNA
<213> Oryza sativa

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<222> (505)
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<220>
<221> unsure
<222> (510)
<223> n is a, c, g or t

<220>
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<222> (545)
<223> n is a, c, g or t

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cgccaacgac gaccacatcc tgacgctgtc atgcccggac aagccgggca tcgtccacgc 180
cgtgactggc atctttgcct cgcggtcggt caacattctt gacctgaagc agttctccga 240
cacggggtcg caaaagttct tcatgcgggt gcactttggc ccagtggccg agacggcgga 300
cctctctgcc gacttctcgg ctctggcgtc gcagtacgac cccatgacct gggacatccg 360
gcccgtggcg caaaagacgc gcgtcctgat atggtgtcaa gatcggcact gtctcaacga 420
cctgctgttc cgcgcccaga gcggccgcct cgccgtcact ggcctcatcg tgtcaacacc 480
cgacttgcgc cctggcgcag cacgngtcan tcgcactgcc gtcacaagaa caagaccaca 540
ggagnagaat ccaactgcaa gac 563

<210> 6
<211> 278
<212> PRT
<213> Oryza sativa

<400> 6
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His Ile Leu Thr Leu Ser Cys Pro Asp Lys Pro Gly Ile Val His Ala
  1               5                  10                  15

Val Thr Gly Ile Phe Ala Ser Arg Ser Val Asn Ile Leu Asp Leu Lys
            20                  25                  30
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```
Gln Phe Ser Asp Thr Gly Ser Gln Lys Phe Phe Met Arg Val His Phe
         35                  40                  45

Gly Pro Val Ala Glu Thr Ala Asp Leu Ser Ala Asp Phe Ser Ala Leu
     50                  55                  60

Ala Ser Gln Tyr Asp Pro Met Thr Trp Asp Ile Arg Pro Val Ala Gln
 65                  70                  75                  80

Lys Thr Arg Val Leu Ile Met Val Ser Lys Ile Gly His Cys Leu Asn
                 85                  90                  95

Asp Leu Leu Phe Arg Ala Gln Ser Gly Arg Leu Ala Val Asp Val Ala
            100                 105                 110

Leu Ile Val Ser Asn His Pro Asp Phe Ala Pro Leu Ala Ala Ser His
        115                 120                 125

Gly Val Glu Phe Arg His Leu Pro Val Thr Lys Glu Thr Lys Thr Gln
    130                 135                 140

Gln Glu Glu Glu Ile Leu Lys Leu Ala Lys Glu Arg Asp Val Glu Leu
145                 150                 155                 160

Ile Val Leu Ala Arg Tyr Met Gln Val Leu Ser Pro Thr Leu Cys Glu
                165                 170                 175

Ala Met Ser Gly Arg Ile Ile Asn Ile His His Ser Phe Leu Pro Ser
            180                 185                 190

Phe Lys Gly Ala Lys Pro Tyr His Gln Ala Tyr Asp Arg Gly Val Lys
        195                 200                 205

Ile Ile Gly Ala Thr Ala His Phe Val Thr Ala Asp Leu Asp Glu Gly
    210                 215                 220

Pro Ile Ile Glu Gln Arg Ile Ser Arg Val Asp His Gly Met Thr Pro
225                 230                 235                 240

Lys Gln Leu Val Asp Glu Gly Ser Ser Ile Glu Ala Leu Val Leu Gly
                245                 250                 255

Ala Ala Val Gln Trp Phe Ala Glu Arg Arg Val Phe Leu Asn Asn Ser
            260                 265                 270

Lys Thr Val Val Phe Asn
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<210> 7
<211> 594
<212> DNA
<213> Triticum aestivum

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<221> unsure
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<222> (374)
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<220>
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<222> (494)
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<220>
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agtcctcgct tcgaagcagg accattgtct gtttgacttg ctgcatagat ggcaagaagg 180
caggcttcca gttgacattc attgtgtgat aagcaaccat gatcgacctg tagataacca 240
tgtgatgcgt tttcttcaag aggcacgaaa tcccctatca ttacttacca acgacttcct 300
gggaataaaa gggaacaaga gatattagaa ttgattgaag atacagattt tgttgtgntg 360
ggcaagatat gcangtaatg tcngaaactt ccttaaacat atgggaaaga tattattata 420
tcacaaggct ccttcctcng tcnaaaggag gatcctctag naggctcaat gctgggtnaa 480
ttgattggtg cacnaccatt tgtacccana cttagcgggc aacatngacc aaggtnaacg 540
gtcccanagg aaattaanac ttgtntnatc tgaaactngg aacatccaca aann 594

<210> 8
<211> 70
<212> PRT
<213> Triticum aestivum

<400> 8
Pro Arg Asp Val Leu Arg Ala Asp Phe Leu Arg Leu Ser Asp Cys Phe
1 5 10 15

Ser Ala Gln Lys Ser Thr Val Arg Val Pro Asp Ile Asp Pro Lys Tyr
20 25 30

Lys Ile Ala Val Leu Ala Ser Lys Gln Asp His Cys Leu Phe Asp Leu
35 40 45

Leu His Arg Trp Gln Glu Gly Arg Leu Pro Val Asp Ile His Cys Val
50 55 60

Ile Ser Asn His Asp Arg
65 70

<210> 9
<211> 543
<212> DNA
<213> Oryza sativa

<220>
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<222> (381)
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<220>
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<220>
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<222> (449)
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<220>
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<222> (466)
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<222> (470)
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<222> (507)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (521)
<223> n is a, c, g or t

<220>
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<222> (524)
<223> n is a, c, g or t

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ctacaaccgt gtccgttaca cgcttgcgtc ttatatcatc aacgagaact caactggtga 180
agtgaaattt agcccaatga ggcgagtatt gttggagatg attgagaaag cgttttcaac 240
cataaacctt gaaacgcaca ctgggaactc acccaaggat tggagtcatt gatgacatgt 300
ccttccaccc cttgaatcaa gccacaatgg aagatgctgc tcaactggct aagactgtgg 360
cctctgacat tggcaacttc ntacaagtcc cagtatcctg tatggagcag cacaccccac 420
tggcaaacct gtgactgcan tacggcgtna actgggctac ttccanccan attcatgggc 480
atccaatggg atgggtcagg taccccntga tatctgcggg naanccagat aagggccagt 540
ttg 543

<210> 10
<211> 296
<212> PRT
<213> Oryza sativa

<400> 10
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1 5 10 15

Ala Ile Thr Arg Ile Gly Gln Lys Asp Pro Glu Val Val Leu Leu Ser
20 25 30

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Lys Phe Glu Asp Asp His Tyr Asn Arg Val Arg Tyr Thr Leu Ala Ser
         35                  40                  45

Tyr Ile Ile Asn Glu Asn Ser Thr Gly Glu Val Lys Phe Ser Pro Met
     50                  55                  60

Arg Arg Val Leu Leu Glu Met Ile Glu Lys Ala Phe Ser Thr Ile Asn
 65                  70                  75                  80

Leu Glu Thr His Thr Gly Thr His Pro Arg Ile Gly Val Ile Asp Asp
                 85                  90                  95

Met Ser Phe His Pro Leu Asn Gln Ala Thr Met Glu Asp Ala Ala Gln
            100                 105                 110

Leu Ala Lys Thr Val Ala Ser Asp Ile Gly Asn Phe Leu Gln Val Pro
        115                 120                 125

Val Phe Leu Tyr Gly Ala Ala His Pro Thr Gly Lys Pro Val Thr Ala
    130                 135                 140

Val Arg Arg Glu Leu Gly Tyr Phe Gln Pro Asn Tyr Met Gly Ile Gln
145                 150                 155                 160

Trp Met Gly Gln Val Leu Pro Asp Ile Leu Pro Val Lys Pro Asp Glu
                165                 170                 175

Gly Pro Asp His Val Ser Arg Glu Arg Gly Ala Ile Met Ile Gly Ala
            180                 185                 190

Ala Pro Leu Pro Leu Asn Tyr Asn Val Pro Val Leu Ser Lys Asp Ile
        195                 200                 205

Pro Thr Ile Arg Arg Ile Thr Arg Arg Val Thr Gly Arg Gly Gly Gly
    210                 215                 220

Leu Pro Thr Val Gln Ala Leu Ala Leu Ser His Gly Asp Asp Cys Thr
225                 230                 235                 240

Glu Ile Ala Cys Phe Leu Asp Pro Asp His Val Ser Ala Asp Gln Val
                245                 250                 255

Gln Gln Gln Val Glu Gln Ile Ala Ala Glu Gln Gly Leu Glu Val Glu
            260                 265                 270

Lys Gly Tyr Phe Thr Asp Phe Ser Lys Asp Ala Met Leu Glu Lys Tyr
        275                 280                 285

Phe Lys Ile Val Leu Ser Val Asp
    290                 295
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<210> 11
<211> 468
<212> DNA
<213> Glycine max

<220>
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<222> (398)
<223> n is a, c, g or t

<220>
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<223> n is a, c, g or t

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<222> (446)
<223> n is a, c, g or t

<220>
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<222> (467)
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attatcttcc atccacttgg tcatgcgtcg ctcgacgagg cagcttggct tgccaaagca 180
gtggcagcag acattggcaa ccgattcagt gtgccagtgt ttctgtacgc cgcagcccac 240
ccaacaggga aggaaagttg atgccataag gcgagagctc ggatattacc ggccaaattc 300
aaggggaagt caatgggccg ggtgggcaat gcccgaaacg ctaccgctga gcctgatgaa 360
gggccaaacg tgggtttcaa gagctaaagg catcacantt gattgggtgc acgccccttg 420
ggnttacatt ctacaacgtt ccaatncctt tgcactgatg tgtcaant 468

<210> 12
<211> 128
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (87)
<223> Xaa can be any naturally ocurring amino acid

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1 5 10 15

Glu Ala Thr Phe Asn Ala Ile Asn Leu Glu Phe His Glu Gly Ala His
20 25 30

Pro Arg Leu Gly Ala Leu Asp Asp Ile Ile Phe His Pro Leu Gly His
35 40 45

Ala Ser Leu Asp Glu Ala Ala Trp Leu Ala Lys Ala Val Ala Ala Asp
50 55 60

Ile Gly Asn Arg Phe Ser Val Pro Val Phe Leu Tyr Ala Ala Ala His
65 70 75 80

Pro Thr Gly Lys Glu Ser Xaa Cys His Lys Ala Arg Ala Arg Ile Leu
85 90 95

Pro Ala Lys Phe Lys Gly Lys Ser Met Gly Arg Val Gly Asn Ala Arg
100 105 110

Asn Ala Thr Ala Glu Pro Asp Glu Gly Pro Asn Val Gly Phe Lys Ser
115 120 125

<210> 13
<211> 416
<212> DNA
<213> Triticum aestivum

<220>
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<222> (393)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (398)
<223> n is a, c, g or t

<220>
<221> unsure
<222> (405)
<223> n is a, c, g or t

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gagtactaca accgtgtccg ctacacgctt gtctcctaca tcaccaacga aagctcgact 180
ggtggagctg tatttagccc aatcaggaag gtactgctgg cgatgatcga ggctgcattt 240
tcagccataa acctcgaagt gcactgtgga actcatccaa ggattggtgt cgtcgatgac 300
atttcattcc acccttgaa tcaagcggac acaatagagg atgctgctca gctggtaagc 360
tggtacctct gacattggaa tggttcaatt cantggtncc aaaangcgga acaata 416

<210> 14
<211> 302
<212> PRT
<213> Triticum aestivum

<400> 14
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1 5 10 15

Ala Val Val Asp Ala Ile Ser Arg Ile Gly Gln Lys Asp Pro Glu Val
20 25 30

Val Leu Leu Asn Lys Phe Glu Asp Glu Tyr Tyr Asn Arg Val Arg Tyr
35 40 45

Thr Leu Val Ser Tyr Ile Thr Asn Glu Ser Ser Thr Gly Gly Ala Val
50 55 60

Phe Ser Pro Ile Arg Lys Val Leu Leu Ala Met Ile Glu Ala Ala Phe
65 70 75 80

Ser Ala Ile Asn Leu Glu Val His Cys Gly Thr His Pro Arg Ile Gly
85 90 95

Val Val Asp Asp Ile Ser Phe His Pro Leu Asn Gln Ala Asp Thr Ile
100 105 110

Glu Asp Ala Ala Gln Leu Ala Lys Leu Val Ala Ser Asp Ile Gly Asn
115 120 125

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Gly Leu Gln Val Pro Val Phe Leu Tyr Ala Ala Ala His Pro Thr Ser
    130                 135                 140

Lys Ser Val Ser Ala Val Arg Arg Glu Leu Gly Tyr Phe Arg Pro Asn
145                 150                 155                 160

His Lys Gly Val Gln Trp Ala Gly Pro Val Leu Pro Asp Thr Leu Pro
                165                 170                 175

Met Lys Pro Asp Val Gly Pro Val His Val Pro Arg Glu Arg Gly Ala
            180                 185                 190

Thr Met Val Gly Ala Gln Pro Leu Val Glu Ser Tyr Asn Val Pro Ile
        195                 200                 205

Phe Cys Lys Asp Val Pro Thr Val Arg Arg Ile Thr Arg Arg Val Thr
    210                 215                 220

Gly Arg Ser Gly Gly Leu Pro Ser Val Gln Ala Leu Ala Leu Phe His
225                 230                 235                 240

Gly Asp Asn Cys Thr Glu Ile Ala Cys Phe Leu Leu Asp Pro Asp His
                245                 250                 255

Val Gly Ala Asp Arg Val Gln Trp Leu Val Glu Gln Ile Ala Glu Glu
            260                 265                 270

Gln Gly Leu Glu Val Glu Lys Gly Tyr Phe Thr Asp Leu Ser Lys His
        275                 280                 285

Met Met Leu Glu Arg Tyr Ser Glu Met Val Ser Ala Ala Asp
    290                 295                 300
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<210> 15
<211> 1076
<212> DNA
<213> Zea mays

<400> 15

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cgccgacgtc cgccgcgagg tcgccgccga tgtggccgcg ctctcgtcgg cccacggact  120
cgtgccgggg ctggccgtgg tcatcgtggg gagcaggaag gactcgcaga cgtacgtgaa  180
catgaagcgc aaggcgtgcg ccgaggtcgg catctgctcc atcgacgtcg acctcccgga  240
ggacatctcc gagaccgcgc tcgtcgccga ggttcatcgc ctcaacgctg accccgcagt  300
gcacgggatc cttgtccagc ttccacttcc taagcatatc aacgaagaga agatactgag  360
cgagatttcc atcgagaaag atgtggatgg cttccatcct ctcaacattg gcaagcttgc  420
aatgaaaggc agagagccac tgttcgtacc atgtacgcca aaggggtgca tggagctctt  480
gtcaaggagc ggagtcactg ttaaaggtaa gcgggcagtt gtggttggtc gcagcaacat  540
cgtcgggcta cctgtatccc tgctccttct gaaggcagat gcgaccgtat ctgttgtgca  600
ctcgcggacc cctgatcctg aaagcattgt acgcgaagct gacatagtca tcgcggcagc  660
tgggcaggct atgatgatca aaggtgactg gatcaagcca ggtgctgcgg tcatcgatgt  720
cgggacgaac tccatcgatg accctacccg gaagtccggg gtacggctcg tcggcgatgt  780
ggatttcgca gcggcgagca aggttgctgg gtacctgact ccggttcccg gaggcgttgg  840
cccaatgacg gtggcaatgc tgctgaagaa cacggtggat ggggcaaagc gggggatagt  900
cgagtagcta cgttcatctc acttcacgtt gctgtacggc ctgtgttgca aggatgtgag  960
ctgactcgaa aagcgtgtgt tggttggtga acaatctgtt tcccaagaat aagaatgata 1020
gtcacagctg ttttcctgtt taataaatgc aatgaagaaa gaattttggc tttaaa     1076
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<210> 16
<211> 290

<212> PRT
<213> Zea mays

<400> 16

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Met Ala Gln Ile Ile Asp Gly Lys Ala Ile Ala Ala Asp Val Arg Arg
  1               5                  10                  15

Glu Val Ala Ala Asp Val Ala Ala Leu Ser Ser Ala His Gly Leu Val
             20                  25                  30

Pro Gly Leu Ala Val Val Ile Val Gly Ser Arg Lys Asp Ser Gln Thr
         35                  40                  45

Tyr Val Asn Met Lys Arg Lys Ala Cys Ala Glu Val Gly Ile Cys Ser
     50                  55                  60

Ile Asp Val Asp Leu Pro Glu Asp Ile Ser Glu Thr Ala Leu Val Ala
 65                  70                  75                  80

Glu Val His Arg Leu Asn Ala Asp Pro Ala Val His Gly Ile Leu Val
                 85                  90                  95

Gln Leu Pro Leu Pro Lys His Ile Asn Glu Glu Lys Ile Leu Ser Glu
            100                 105                 110

Ile Ser Ile Glu Lys Asp Val Asp Gly Phe His Pro Leu Asn Ile Gly
        115                 120                 125

Lys Leu Ala Met Lys Gly Arg Glu Pro Leu Phe Val Pro Cys Thr Pro
    130                 135                 140

Lys Gly Cys Met Glu Leu Leu Ser Arg Ser Gly Val Thr Val Lys Gly
145                 150                 155                 160

Lys Arg Ala Val Val Val Gly Arg Ser Asn Ile Val Gly Leu Pro Val
                165                 170                 175

Ser Leu Leu Leu Leu Lys Ala Asp Ala Thr Val Ser Val Val His Ser
            180                 185                 190

Arg Thr Pro Asp Pro Glu Ser Ile Val Arg Glu Ala Asp Ile Val Ile
        195                 200                 205

Ala Ala Ala Gly Gln Ala Met Met Ile Lys Gly Asp Trp Ile Lys Pro
    210                 215                 220

Gly Ala Ala Val Ile Asp Val Gly Thr Asn Ser Ile Asp Asp Pro Thr
225                 230                 235                 240

Arg Lys Ser Gly Val Arg Leu Val Gly Asp Val Asp Phe Ala Ala Ala
                245                 250                 255

Ser Lys Val Ala Gly Tyr Leu Thr Pro Val Pro Gly Gly Val Gly Pro
            260                 265                 270

Met Thr Val Ala Met Leu Leu Lys Asn Thr Val Asp Gly Ala Lys Arg
        275                 280                 285

Gly Ile
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<213> Oryza sativa

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gaaggatgca attggggttg tgcctgggct ggcagtcatc ctagttgggt caaggaagga 180
ttctcaaacg tatgtgcgca acaagaagaa ggcatgcgaa gcggttggta tcaagtcata 240
tgaggttaat ttgccggaag acagctctga ggatgaggtt ctcaagcaca tcgcaacatt 300
taacagtgat ccgtcngtgc atggcatctt ggtcagttcc cctacctcat catatgaatg 360
atgagaacat tttgaatgct gtagtattga gaaggatgtt gatggattca ncactgaaca 420
ttggcgactg catgcaagcc ggatcgtcct tgtccagcac cctaagatca tggatacacc 480
agatatggan tgaatcaagg aanaactttg tattggcggg nattttggga tctgcgctat 540
acgcaaanca ccacgtacat gnatcaatca gaaccggga 579

<210> 18
<211> 292
<212> PRT
<213> Oryza sativa

<400> 18

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Ala Lys Ile Ile Asp Gly Lys Leu Val Ala Lys Gln Ile Arg Glu Glu
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Ile Ala Val Glu Ile Ala Lys Met Lys Asp Ala Ile Gly Val Val Pro
             20                  25                  30

Gly Leu Ala Val Ile Leu Val Gly Ser Arg Lys Asp Ser Gln Thr Tyr
         35                  40                  45

Val Arg Asn Lys Lys Lys Ala Cys Glu Ala Val Gly Ile Lys Ser Tyr
     50                  55                  60

Glu Val Asn Leu Pro Glu Asp Ser Ser Glu Asp Glu Val Leu Lys His
 65                  70                  75                  80

Ile Ala Thr Phe Asn Ser Asp Pro Ser Val His Gly Ile Leu Val Gln
                 85                  90                  95

Leu Pro Leu Pro His His Met Asn Asp Glu Asn Ile Leu Asn Ala Val
            100                 105                 110

Ser Ile Glu Lys Asp Val Asp Gly Phe His Pro Leu Asn Ile Gly Arg
        115                 120                 125

Leu Ala Met Gln Gly Arg Asp Pro Phe Phe Val Pro Cys Thr Pro Lys
    130                 135                 140

Gly Cys Met Glu Leu Leu His Arg Tyr Gly Val Glu Ile Lys Gly Lys
145                 150                 155                 160

Arg Ala Val Val Ile Gly Arg Ser Asn Ile Val Gly Met Pro Ala Ala
                165                 170                 175

Leu Leu Leu Gln Lys Ala Asn Ala Thr Val Ser Ile Val His Ser Asn
            180                 185                 190

Thr Lys Lys Pro Glu Glu Ile Thr Arg Gln Ala Asp Ile Val Ile Ala
        195                 200                 205

Ala Val Gly Val Ala Asn Leu Val Arg Gly Ser Trp Ile Lys Pro Gly
    210                 215                 220

Ala Ala Ile Ile Asp Val Gly Ile Asn Pro Val Asp Asp Pro Glu Ser
225                 230                 235                 240

Pro Arg Gly Tyr Arg Leu Val Gly Asp Val Cys Tyr Glu Glu Ala Ser
                245                 250                 255

Lys Ile Ala Gly Leu Ile Thr Pro Val Pro Gly Gly Val Gly Pro Met
            260                 265                 270

Thr Ile Ala Met Leu Leu Ser Asn Thr Leu Glu Ser Ala Lys Arg Ile
        275                 280                 285

His Lys Phe Lys
    290
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ttcatggcat cctcgttcag ttacccttac cttcgcatat gaatgagcag aacatcttga 180
acgctgtcag gattgagaag gatgtagatg gttttcatcc gttaaatatt ggtcgtcttg 240
ccatgcgtgg aagagaacct ctgtttgttc cttgtacacc aaagggatgc atagagctac 300
tgcacagata caatgtttct attaaaggaa agagggctgt tgtgattggt cggagcaata 360
ttgttggaat gccagctgct ctcttgcttc aaagggaaga tgctactgtc agtattgtcc 420
attctagaac cagtaacccc gaagagatca taagacaggc agatattatc attgctgctg 480
ttgggcaagc aaacatggtg aggggaagct ggataaagcc tggtgcagtc attattgatg 540
ttggaatcaa cccggtagag gatccaaata gcccccgagg ttacaaactg gtgggagatg 600
tttgttatga agaagccata agaattgcct ctgctgttac accagttcct ggaggagttg 660
gtccaatgac catagcaatg cttctacaaa atacactcat ctctgcaaag agggtgcaca 720
attttgaata acattgtgaa agggtgttgt ataccattat gagccatcaa tttttgttta 780
ggtgactcgt ggatttaagg tagggttttt tcaacattgg gacttaagcc ccaaataaga 840
gaaaatgttg ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaca aaaaaaaaaa 900
acttgagggg gccccggacc caatat 926

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<211> 242
<212> PRT
<213> Glycine max

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20 25 30

Gly Tyr Asn Asp Asp Pro Ser Val His Gly Ile Leu Val Gln Leu Pro
35 40 45

Leu Pro Ser His Met Asn Glu Gln Asn Ile Leu Asn Ala Val Arg Ile
50 55 60

Glu Lys Asp Val Asp Gly Phe His Pro Leu Asn Ile Gly Arg Leu Ala
65 70 75 80

Met Arg Gly Arg Glu Pro Leu Phe Val Pro Cys Thr Pro Lys Gly Cys
85 90 95

Ile Glu Leu Leu His Arg Tyr Asn Val Ser Ile Lys Gly Lys Arg Ala
100 105 110

Val Val Ile Gly Arg Ser Asn Ile Val Gly Met Pro Ala Ala Leu Leu
115 120 125

Leu Gln Arg Glu Asp Ala Thr Val Ser Ile Val His Ser Arg Thr Ser
130 135 140

Asn Pro Glu Glu Ile Ile Arg Gln Ala Asp Ile Ile Ile Ala Ala Val
145 150 155 160

Gly Gln Ala Asn Met Val Arg Gly Ser Trp Ile Lys Pro Gly Ala Val
165 170 175

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Ile Ile Asp Val Gly Ile Asn Pro Val Glu Asp Pro Asn Ser Pro Arg
            180                 185                 190

Gly Tyr Lys Leu Val Gly Asp Val Cys Tyr Glu Glu Ala Ile Arg Ile
        195                 200                 205

Ala Ser Ala Val Thr Pro Val Pro Gly Gly Val Gly Pro Met Thr Ile
    210                 215                 220

Ala Met Leu Leu Gln Asn Thr Leu Ile Ser Ala Lys Arg Val His Asn
225                 230                 235                 240

Phe Glu
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ggcggtggtg atcgtgggga gcaggaagga ctcgcagacg tacgtgcaga tgaagcgcaa 180
ggcctgcgcc gaggtcggca tccgctcctt cgacgtcgac ctccccgagg acatcgccga 240
ggccgcgctc gtcgccgagg tccaccgcct caacgccgac cccgccgtcc acggaattct 300
tgttcagctt ccattgccca agcatatcaa cgaagaaaat atcttaaacc agatctccat 360
tgagaaagat gtcgacggct ttcatccttt gaacattggc aagcttgcaa tgaaaggcag 420
agatccactg ttcgtacctt gcacgccaaa gggatgcatg gagctcctgt cacgaagtgg 480
cgtcactgta aaaggaaaac acgcagttgt ggttgggcgt agcaacatcg tgggtttacc 540

aagtatccct tctccttctg aaagcggacg ctaccgtgtc gatngtgcat caacggaccc 600
aaatccccaa acaatttccg tcaagcaaga cattgtcatt gcagcagctg ggcaagccat 660
gatgatcaag ggagactggn ttaaacaaaa gcgcaacgnc atcnacgtcg ggacaatcca 720
tcgacgacca acaagaatct gggtaaaatc cttggnagtg gttctcngag naacaagccn 780
ggtcactgat cggcccggan gntcggccat actggnattt ctaaaaaagg gganggncaa 840
anggannсac gattcgcnna ttgaagggan attna 875

<210> 22
<211> 289
<212> PRT
<213> Triticum aestivum

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Ala Glu Ile Arg Arg Glu Ile Gly Ala Glu Val Ala Val Leu Ser Ser
             20                  25                  30

Ala His Asn Ile Val Pro Gly Leu Ala Val Val Ile Val Gly Ser Arg
         35                  40                  45

Lys Asp Ser Gln Thr Tyr Val Gln Met Lys Arg Lys Ala Cys Ala Glu
     50                  55                  60

Val Gly Ile Arg Ser Phe Asp Val Asp Leu Pro Glu Asp Ile Ala Glu
 65                  70                  75                  80

Ala Ala Leu Val Ala Glu Val His Arg Leu Asn Ala Asp Pro Ala Val
                 85                  90                  95

His Gly Ile Leu Val Gln Leu Pro Leu Pro Lys His Ile Asn Glu Glu
            100                 105                 110

Asn Ile Leu Asn Gln Ile Ser Ile Glu Lys Asp Val Asp Gly Phe His
        115                 120                 125

Pro Leu Asn Ile Gly Lys Leu Ala Met Lys Gly Arg Asp Pro Leu Phe
    130                 135                 140

Val Pro Cys Thr Pro Lys Gly Cys Met Glu Leu Leu Ser Arg Ser Gly
145                 150                 155                 160

Val Thr Val Lys Gly Lys His Ala Val Val Val Gly Arg Ser Asn Ile
                165                 170                 175

Val Gly Leu Pro Ser Ile Pro Ser Pro Ser Glu Ser Gly Arg Tyr Arg
            180                 185                 190

Val Asp Xaa Ala Ser Thr Asp Pro Asn Pro Gln Thr Ile Ser Val Lys
        195                 200                 205

Gln Asp Ile Val Ile Ala Ala Ala Gly Gln Ala Met Met Ile Lys Gly
    210                 215                 220

Asp Trp Xaa Lys Gln Lys Arg Asn Xaa Ile Xaa Val Gly Thr Ile His
225                 230                 235                 240
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Arg Arg Pro Thr Arg Ile Trp Val Lys Ser Leu Xaa Val Val Leu Xaa
                245                 250                 255

Xaa Thr Ser Xaa Val Thr Asp Arg Pro Gly Xaa Ser Ala Ile Leu Xaa
            260                 265                 270

Phe Leu Lys Lys Gly Xaa Xaa Lys Xaa Xaa His Asp Ser Xaa Ile Glu
        275                 280                 285

Gly
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